

(i) APPLICANT:

(ii) TITLE OF INVENTION:

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 60 State Street, Suite 510

(C) CITY: Boston

(D) STATE: MA

(E) \ COUNTRY: USA

(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: ASCII (text)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/

(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/

(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.

(B) REGISTRATION NUMBER: 36,709

(C) REFERENCE/DOCKET NUMBER: CPI-004DVCP3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400

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sub
A2

[illegible]

TACACTCCTT	GCCACAGTCT	GGCAGAAAGA	ATCAAAC TTC	AGAGACTCCT	CCGGCCAGTT	60										
G TAGACACTA	TCCTTG TCAA	GTGTGCAGAT	CCAACAGCCG	CACGAGTCAG	CTGTCCATAT	120										
CTACAGTGCT	GGA ACTCTGC	AAGGGCCAAG	CAGGAGAGCT	GGCGGTTGGG	AGAGAAATAC	180										
TTAAAGCTGG	GTCCATCGGG	GTTGGTGGTG	TCGATTACGT	CTTAAGTTGT	ATCCTTGGAA	240										
ACCAAGCTGA	ATCAAACAAC	TGGCAAGAAC	TGCTGGGTCG	CCTCTGTCTT	ATAGACAGGT	300										
TGCTGTTGGA	ATTTCTGCT	GAATTCTATC	CTCATATTGT	CAGTACTGAT	GTCTCACAAG	360										
CTGAGCCTGT	TGAAATCAGG	TACAAGAAGC	TGCTCTCCCT	CTTAACCTTT	GCCTTGCAAT	420										
CCATTGACAA	TTCCCACTCG	ATGGTTGGCA	AGCTCTCTCG	GAGGATATAT	CTGAGCTCTG	480										
CCAGG	ATG	GTG	ACC	GCA	GTG	CCC	GCT	GTG	TTT	TCC	AAG	CTG	GTA	ACC	527	
	Met	Val	Thr	Ala	Val	Pro	Ala	Val	Phe	Ser	Lys	Leu	Val	Thr		
	1				5					10						
ATG	CTT	AAT	GCT	TCT	GGC	TCC	ACC	CAC	TTC	ACC	AGG	ATG	CGC	CGG	CGT	575
Met	Leu	Asn	Ala	Ser	Gly	Ser	Thr	His	Phe	Thr	Arg	Met	Arg	Arg	Arg	
	15				20					25					30	
CTG	ATG	GCT	ATC	GCG	GAT	GAG	GTA	GAA	ATT	GCC	GAG	GTC	ATC	CAG	CTG	623
Leu	Met	Ala	Ile	Ala	Asp	Glu	Val	Glu	Ile	Ala	Glu	Val	Ile	Gln	Leu	
				35					40					45		
GGT	GTG	GAG	GAC	ACT	GTG	GAT	GGG	CAT	CAG	GAC	AGC	TTA	CAG	GCC	GTG	671
Gly	Val	Glu	Asp	Thr	Val	Asp	Gly	His	Gln	Asp	Ser	Leu	Gln	Ala	Val	
			50					55					60			
GCC	CCC	ACC	AGC	TGT	CTA	GAA	AAC	AGC	TCC	CTT	GAG	CAC	ACA	GTC	CAT	719
Ala	Pro	Thr	Ser	Cys	Leu	Glu	Asn	Ser	Ser	Leu	Glu	His	Thr	Val	His	
		65					70					75				
AGA	GAG	AAA	ACT	GGA	AAA	GGA	CTA	AGT	GCT	ACG	AGA	CTG	AGT	GCC	AGC	767
Arg	Glu	Lys	Thr	Gly	Lys	Gly	Leu	Ser	Ala	Thr	Arg	Leu	Ser	Ala	Ser	
	80					85					90					

TCG Ser 95	GAG Glu	GAC Asp	ATT Ile	TCT Ser	GAC Asp 100	AGA Arg	CTG Leu	GCC Ala	GGC Gly	GTC Val 105	TCT Ser	GTA Val	GGA Gly	CTT Leu	CCC Pro 110	815
AGC Ser	TCA Ser	ACA Thr	ACA Thr	ACA Thr 115	GAA Glu	CAA Gln	CCA Pro	AAG Lys	CCA Pro 120	GCG Ala	GTT Val	CAA Gln	ACA Thr	AAA Lys 125	GGC Gly	863
AGA Arg	CCC Pro	CAC His	AGT Ser 130	CAG Gln	TGT Cys	TTG Leu	AAC Asn 135	TCC Ser	TCC Ser	CCT Pro	TTG Leu	TCT Ser	CAT His 140	GCT Ala	CAA Gln	911
TTA Leu	ATG Met	TTC Phe 145	CCA Pro	GCA Ala	CCA Pro	TCA Ser	GCC Ala 150	CCT Pro	TGT Cys	TCC Ser	TCT Ser	GCC Ala 155	CCG Pro	TCT Ser	GTC Val	959
CCA Pro 160	GAT Asp	ATT Ile	TCT Ser	AAG Lys	CAC His	AGA Arg 165	CCC Pro	CAG Gln	GCA Ala	TTT Phe 170	GTT Val	CCC Pro	TGC Cys	AAA Lys	ATA Ile	1007
CCT Pro 175	TCC Ser	GCA Ala	TCT Ser	CCT Pro	CAG Gln 180	ACA Thr	CAG Gln	CGC Arg	AAG Lys	TTC Phe 185	TCT Ser	CTA Leu	CAA Gln	TTC Phe	CAG Gln 190	1055
AGG Arg	AAC Asn	TGC Cys	TCT Ser 195	GAA Glu	CAC His	CGA Arg	GAC Asp	TCA Ser	GAC Asp 200	CAG Gln	CTC Leu	TCC Ser	CCA Pro	GTC Val 205	TTC Phe	1103
ACT Thr	CAG Gln	TCA Ser	AGA Arg 210	CCC Pro	CCA Pro	CCC Pro	TCC Ser	AGT Ser 215	AAC Asn	ATA Ile	CAC His	AGG Arg 220	CCA Pro	AAG Lys	CCA Pro	1151
TCC Ser	CGA Arg 225	CCC Pro	GTT Val	CCG Pro	GGC Gly	AGT Ser	ACA Thr 230	AGC Ser	AAA Lys	CTA Leu	GGG Gly	GAC Asp 235	GCC Ala	ACA Thr	AAA Lys	1199
AGT Ser 240	AGC Ser	ATG Met	ACA Thr	CTT Leu	GAT Asp 245	CTG Leu	GGC Gly	AGT Ser	GCT Ala	TCC Ser 250	AGG Arg	TGT Cys	GAC Asp	GAC Asp	AGC Ser	1247
TTT Phe 255	GGC Gly	GGC Gly	GGC Gly	GGC Gly	AAC Asn 260	AGT Ser	GGC Gly	AAC Asn	GCC Ala	GTC Val 265	ATA Ile	CCC Pro	AGC Ser	GAC Asp	GAG Glu 270	1295
ACA Thr	GTG Val	TTC Phe	ACG Thr 275	CCG Pro	GTG Val	GAG Glu	GAC Asp	AAG Lys	TGC Cys	AGG Arg 280	TTA Leu	GAT Asp	GTG Val	AAC Asn 285	ACC Thr	1343
GAG Glu	CTC Leu	AAC Asn	TCC Ser 290	AGC Ser	ATC Ile	GAG Glu	GAC Asp	CTT Leu 295	CTT Leu	GAA Glu	GCA Ala	TCC Ser 300	ATG Met	CCT Pro	TCA Ser	1391
AGT Ser	GAC Asp 305	ACG Thr	ACA Thr	GTC Val	ACT Thr	TTC Phe	AAG Lys 310	TCC Ser	GAA Glu	GTC Val	GCC Ala	GTC Val 315	CTC Leu	TCT Ser	CCG Pro	1439

GAA	AAG	GCC	GAA	AAT	GAC	GAC	ACC	TAC	AAA	GAC	GAC	GTC	AAT	CAT	AAT	1487
Glu	Lys	Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	
320						325					330					
CAA	AAG	TGC	AAA	GAA	AAG	ATG	GAA	GCT	GAA	GAG	GAG	GAG	GCT	TTA	GCG	1535
Gln	Lys	Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu	Glu	Ala	Leu	Ala	
335					340					345					350	
No 1																
ATC	GCC	ATG	GCG	ATG	TCA	GCG	TCT	CAG	GAT	GCC	CTC	CCC	ATC	GTC	CCT	1583
Ile	Ala	Met	Ala	Met	Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	
		353		355					360					365		
CAG	CTG	CAG	GTG	GAA	AAT	GGA	GAA	GAT	ATT	ATC	ATC	ATT	CAG	CAG	GAC	1631
Gln	Leu	Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	
			370					375					380			
ACA	CCA	GAA	ACT	CTT	CCA	GGA	CAT	ACC	AAA	GCG	AAA	CAG	CCT	TAC	AGA	1679
Thr	Pro	Glu	Thr	Leu	Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	
		385					390					395				
GAA	GAC	GCT	GAG	TGG	CTG	AAA	GGC	CAG	CAG	ATA	GGC	CTC	GGA	GCA	TTT	1727
Glu	Asp	Ala	Glu	Trp	Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	
	400					405					410					
TCT	TCC	TGT	TAC	CAA	GCA	CAG	GAT	GTG	GGG	ACT	GGG	ACT	TTA	ATG	GCT	1775
Ser	Ser	Cys	Tyr	Gln	Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	
415					420					425					430	
GTG	AAA	CAG	GTG	ACG	TAC	GTC	AGA	AAC	ACA	TCC	TCC	GAG	CAG	GAG	GAG	1823
Val	Lys	Gln	Val	Thr	Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	
				435					440					445		
GTG	GTG	GAA	GCG	TTG	AGG	GAA	GAG	ATC	CGG	ATG	ATG	GGT	CAC	CTC	AAC	1871
Val	Val	Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	Met	Gly	His	Leu	Asn	
			450					455					460			
CAT	CCA	AAC	ATC	ATC	CGG	ATG	CTG	GGG	GCC	ACG	TGC	GAG	AAG	AGC	AAC	1919
His	Pro	Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	Cys	Glu	Lys	Ser	Asn	
		465					470					475				
TAC	AAC	CTC	TTC	ATT	GAG	TGG	ATG	GCG	GGA	GGA	TCT	GTG	GCT	CAC	CTC	1967
Tyr	Asn	Leu	Phe	Ile	Glu	Trp	Met	Ala	Gly	Gly	Ser	Val	Ala	His	Leu	
	480					485					490					
TTG	AGT	AAA	TAC	GGA	GCT	TTC	AAG	GAG	TCA	GTC	GTC	ATT	AAC	TAC	ACT	2015
Leu	Ser	Lys	Tyr	Gly	Ala	Phe	Lys	Glu	Ser	Val	Val	Ile	Asn	Tyr	Thr	
495					500					505					510	
GAG	CAG	TTA	CTG	CGT	GGC	CTT	TCC	TAT	CTC	CAC	GAG	AAC	CAG	ATC	ATT	2063
Glu	Gln	Leu	Leu	Arg	Gly	Leu	Ser	Tyr	Leu	His	Glu	Asn	Gln	Ile	Ile	
	</															

[illegible]

AAATTCTACG TGCTGTGTGA CTATGACTCC TAAGACTTCC AGGGCTTAAG GGCTAACTCC 3211
 TATTAGCACC TTACTATGTA AGCAAATGCT ACAAAAAAAAAA AAAAAAAAAA 3260

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 AA
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Thr Ala Val Pro Ala Val Phe Ser Lys Leu Val Thr Met Leu
 1 5 10 15
 Asn Ala Ser Gly Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met
 20 25 30
 Ala Ile Ala Asp Glu Val Glu Ile Ala Glu Val Ile Gln Leu Gly Val
 35 40 45
 Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu Gln Ala Val Ala Pro
 50 55 60
 Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His Thr Val His Arg Glu
 65 70 75 80
 Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu Ser Ala Ser Ser Glu
 85 90 95
 Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val Gly Leu Pro Ser Ser
 100 105 110
 Thr Thr Thr Glu Gln Pro Lys Pro Ala Val Gln Thr Lys Gly Arg Pro
 115 120 125
 His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His Ala Gln Leu Met
 130 135 140
 Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala Pro Ser Val Pro Asp
 145 150 155 160
 Ile Ser Lys His Arg Pro Gln Ala Phe Val Pro Cys Lys Ile Pro Ser
 165 170 175
 Ala Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe Gln Arg Asn
 180 185 190
 Cys Ser Glu His Arg Asp Ser Asp Gln Leu Ser Pro Val Phe Thr Gln
 195 200 205
 Ser Arg Pro Pro Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg
 210 215 220

009608890.063000

Pro	Val	Pro	Gly	Ser	Thr	Ser	Lys	Leu	Gly	Asp	Ala	Thr	Lys	Ser	Ser
225						230				235					240
Met	Thr	Leu	Asp	Leu	Gly	Ser	Ala	Ser	Arg	Cys	Asp	Asp	Ser	Phe	Gly
				245					250					255	
Gly	Gly	Gly	Asn	Ser	Gly	Asn	Ala	Val	Ile	Pro	Ser	Asp	Glu	Thr	Val
			260					265					270		
Phe	Thr	Pro	Val	Glu	Asp	Lys	Cys	Arg	Leu	Asp	Val	Asn	Thr	Glu	Leu
		275					280					285			
Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro	Ser	Ser	Asp
	290					295					300				
Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu	Ser	Pro	Glu	Lys
305					310					315					320
Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	Gln	Lys
				325					330					335	
Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Ala
			340					345					350		
Met	Ala	Met	Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	Gln	Leu
		355					360					365			
Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	Thr	Pro
	370					375					380				
Glu	Thr	Leu	Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	Glu	Asp
385					390					395					400
Ala	Glu	Trp	Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	Ser	Ser
				405					410					415	
Cys	Tyr	Gln	Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	Val	Lys
			420					425					430		
Gln	Val	Thr	Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	Val	Val
		435					440					445			
Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	Met	Gly	His	Leu	Asn	His	Pro
	450					455					460				
Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	Cys	Glu	Lys	Ser	Asn	Tyr	Asn
465					470					475					480
Leu	Phe	Ile	Glu	Trp	Met	Ala	Gly	Gly	Ser	Val	Ala	His	Leu	Leu	Ser
				485					490					495	
Lys	Tyr	Gly	Ala	Phe	Lys	Glu	Ser	Val	Val	Ile	Asn	Tyr	Thr	Glu	Gln
			500					505					510		

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 5539 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

48

CGG	AGC	CCC	GCG	GGG	GCG	GAG	CCG	CCC	TCT	GCA	GCG	GCC	CCC	TCC	GGT	768
Arg	Ser	Pro	Ala	Gly	Ala	Glu	Pro	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Gly	
				245					250					255		
CGA	GAG	ATG	GAG	AAT	AAA	GAA	ACC	CTC	AAA	GGA	CTG	CAC	AAG	ATG	GAG	816
Arg	Glu	Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	His	Lys	Met	Glu	
				260					265					270		
GAT	CGC	CCG	GAG	GAG	AGA	ATG	ATC	CGG	GAG	AAG	CTC	AAG	GCG	ACC	TGT	864
Asp	Arg	Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	Lys	Ala	Thr	Cys	
				275					280					285		
ATG	CCG	GCC	TGG	AAG	CAC	GAG	TGG	TTG	GAG	AGG	AGG	AAC	AGG	AGA	GGC	912
Met	Pro	Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Arg	Asn	Arg	Arg	Gly	
				290					295					300		
CCT	GTG	GTG	GTG	AAG	CCA	ATC	CCT	ATT	AAA	GGA	GAT	GGA	TCT	GAA	GTG	960
Pro	Val	Val	Val	Lys	Pro	Ile	Pro	Ile	Lys	Gly	Asp	Gly	Ser	Glu	Val	
				305					310					315		
AAT	AAC	TTG	GCA	GCT	GAG	CCC	CAG	GGA	GAG	GGC	CAG	GCA	GGT	TCC	GCT	1008
Asn	Asn	Leu	Ala	Ala	Glu	Pro	Gln	Gly	Glu	Gly	Gln	Ala	Gly	Ser	Ala	
				325					330					335		
GCA	CCA	GCC	CCC	AAG	GGC	CGA	CGA	AGC	CCA	TCT	CCT	GGC	AGC	TCT	CCG	1056
Ala	Pro	Ala	Pro	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	Gly	Ser	Ser	Pro	
				340					345					350		
TCA	GGG	CGC	TCG	GTG	AAG	CCG	GAA	TCC	CCA	GGA	GTA	AGA	CGG	AAA	CGA	1104
Ser	Gly	Arg	Ser	Val	Lys	Pro	Glu	Ser	Pro	Gly	Val	Arg	Arg	Lys	Arg	
				355					360					365		
GTG	TCC	CCG	GTG	CCT	TTC	CAG	AGT	GGC	AGA	ATC	ACA	CCA	CCC	CGA	AGA	1152
Val	Ser	Pro	Val	Pro	Phe	Gln	Ser	Gly	Arg	Ile	Thr	Pro	Pro	Arg	Arg	
				370					375					380		
GCC	CCA	TCA	CCG	GAT	GGC	TTC	TCC	CCG	TAC	AGC	CCA	GAG	GAG	ACG	AGC	1200
Ala	Pro	Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	Glu	Glu	Thr	Ser	
				385					390					395		
CGC	CGC	GTG	AAC	AAA	GTG	ATG	AGA	GCC	AGG	CTG	TAC	CTG	CTG	CAG	CAG	1248
Arg	Arg	Val	Asn	Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr	Leu	Leu	Gln	Gln	
				405					410					415		
ATA	GGA	CCC	AAC	TCT	TTC	CTG	ATT	GGA	GGA	GAC	AGT	CCA	GAC	AAT	AAA	1296
Ile	Gly	Pro	Asn	Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser	Pro	Asp	Asn	Lys	
				420					425					430		
TAC	CGG	GTG	TTT	ATT	GGG	CCA	CAG	AAC	TGC	AGC	TGT	GGG	CGT	GGA	GCA	1344
Tyr	Arg	Val	Phe	Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys	Gly	Arg	Gly	Ala	
				435					440					445		
TTC	TGT	ATT	CAC	CTC	TTG	TTT	GTC	ATG	CTC	CGG	GTG	TTT	CAG	CTA	GAA	1392
Phe	Cys	Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val	Phe	Gln	Leu	Glu	
				450					455					460		

CCC Pro 465	TCT Ser	GAC Asp	CCC Pro	ATG Met	TTA Leu	TGG Trp	AGA Arg	AAA Lys	ACT Thr	TTA Leu	AAA Lys	AAT Asn	TTC Phe	GAG Glu	GTT Val	1440
				470								480				
GAG Glu	AGT Ser	TTG Leu	TTC Phe	CAG Gln	AAA Lys	TAC Tyr	CAC His	AGT Ser	AGG Arg	CGT Arg	AGC Ser	TCG Ser	AGA Arg	ATC Ile	AAA Lys	1488
				485								495				
GCT Ala	CCA Pro	TCC Ser	CGG Arg	AAC Asn	ACC Thr	ATC Ile	CAG Gln	AAG Lys	TTT Phe	GTG Val	TCA Ser	CGC Arg	ATG Met	TCA Ser	AAT Asn	1536
				500								510				
TCT Ser	CAC His	ACA Thr	CTG Leu	TCA Ser	TCG Ser	TCT Ser	AGC Ser	ACA Thr	TCC Ser	ACA Thr	TCT Ser	AGT Ser	TCA Ser	GAA Glu	AAC Asn	1584
				515								525				
AGC Ser	ATC Ile	AAG Lys	GAT Asp	GAA Glu	GAG Glu	GAG Glu	CAG Gln	ATG Met	TGT Cys	CCC Pro	ATC Ile	TGC Cys	TTG Leu	CTG Leu	GGC Gly	1632
				530								540				
ATG Met	CTG Leu	GAT Asp	GAG Glu	GAG Glu	AGC Ser	CTG Leu	ACT Thr	GTG Val	TGT Cys	GAA Glu	GAT Asp	GGC Gly	TGC Cys	AGG Arg	AAC Asn	1680
				545								555				
AAG Lys	CTG Leu	CAC His	CAC His	CAT His	TGC Cys	ATG Met	TCC Ser	ATC Ile	TGG Trp	GCG Ala	GAA Glu	GAG Glu	TGT Cys	AGA Arg	AGA Arg	1728
				565								575				
AAT Asn	AGA Arg	GAG Glu	CCT Pro	TTA Leu	ATA Ile	TGT Cys	CCC Pro	CTT Leu	TGT Cys	AGA Arg	TCT Ser	AAG Lys	TGG Trp	AGA Arg	TCC Ser	1776
				580								590				
CAT His	GAC Asp	TTC Phe	TAC Tyr	AGC Ser	CAT His	GAG Glu	TTA Leu	TCA Ser	AGC Ser	CCC Pro	GTG Val	GAG Glu	TCC Ser	CCC Pro	GCC Ala	1824
				595								605				
TCC Ser	CTG Leu	CGA Arg	GCT Ala	GTC Val	CAG Gln	CAG Gln	CCA Pro	TCC Ser	TCC Ser	CCG Pro	CAG Gln	CAG Gln	CCC Pro	GTG Val	GCC Ala	1872
				610								620				
GGA Gly	TCA Ser	CAG Gln	CGG Arg	AGG Arg	AAT Asn	CAG Gln	GAG Glu	AGC Ser	AGT Ser	TTT Phe	AAC Asn	CTT Leu	ACT Thr	CAT His	TTT Phe	1920
				625								635				
GGA Gly	ACC Thr	CAG Gln	CAG Gln	ATT Ile	CCT Pro	TCC Ser	GCT Ala	TAC Tyr	AAA Lys	GAT Asp	TTG Leu	GCC Ala	GAG Glu	CCA Pro	TGG Trp	1968
				645								655				
ATT Ile	CAG Gln	GTG Val	TTT Phe	GGA Gly	ATG Met	GAA Glu	CTC Leu	GTT Val	GGC Gly	TGC Cys	TTA Leu	TTC Phe	TCT Ser	AGA Arg	AAC Asn	2016
				660								670				
TGG Trp	AAC Asn	GTA Val	AGG Arg	GAA Glu	ATG Met	GCC Ala	CTT Leu	AGG Arg	CGT Arg	CTT Leu	TCC Ser	CAC His	GAC Asp	GTT Val	AGT Ser	2064
				675								685				

CGG	AGG	ATA	TAT	CTG	AGC	TCT	GCC	AGG	ATG	GTG	ACC	GCA	GTG	CCC	GCT	2784
Arg	Arg	Ile	Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Ala	Val	Pro	Ala	
		915					920					925				
GTG	TTT	TCC	AAG	CTG	GTA	ACC	ATG	CTT	AAT	GCT	TCT	GGC	TCC	ACC	CAC	2832
Val	Phe	Ser	Lys	Leu	Val	Thr	Met	Leu	Asn	Ala	Ser	Gly	Ser	Thr	His	
	930						935				940					
TTC	ACC	AGG	ATG	CGC	CGG	CGT	CTG	ATG	GCT	ATC	GCG	GAT	GAG	GTA	GAA	2880
Phe	Thr	Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Ile	Ala	Asp	Glu	Val	Glu	
	945					950				955					960	
ATT	GCC	GAG	GTC	ATC	CAG	CTG	GGT	GTG	GAG	GAC	ACT	GTG	GAT	GGG	CAT	2928
Ile	Ala	Glu	Val	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Val	Asp	Gly	His	
				965					970					975		
CAG	GAC	AGC	TTA	CAG	GCC	GTG	GCC	CCC	ACC	AGC	TGT	CTA	GAA	AAC	AGC	2976
Gln	Asp	Ser	Leu	Gln	Ala	Val	Ala	Pro	Thr	Ser	Cys	Leu	Glu	Asn	Ser	
			980					985					990			
TCC	CTT	GAG	CAC	ACA	GTC	CAT	AGA	GAG	AAA	ACT	GGA	AAA	GGA	CTA	AGT	3024
Ser	Leu	Glu	His	Thr	Val	His	Arg	Glu	Lys	Thr	Gly	Lys	Gly	Leu	Ser	
		995					1000					1005				
GCT	ACG	AGA	CTG	AGT	GCC	AGC	TCG	GAG	GAC	ATT	TCT	GAC	AGA	CTG	GCC	3072
Ala	Thr	Arg	Leu	Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Asp	Arg	Leu	Ala	
	1010						1015				1020					
GGC	GTC	TCT	GTA	GGA	CTT	CCC	AGC	TCA	ACA	ACA	ACA	GAA	CAA	CCA	AAG	3120
Gly	Val	Ser	Val	Gly	Leu	Pro	Ser	Ser	Thr	Thr	Thr	Glu	Gln	Pro	Lys	
	1025					1030					1035				1040	
CCA	GCG	GTT	CAA	ACA	AAA	GGC	AGA	CCC	CAC	AGT	CAG	TGT	TTG	AAC	TCC	3168
Pro	Ala	Val	Gln	Thr	Lys	Gly	Arg	Pro	His	Ser	Gln	Cys	Leu	Asn	Ser	
				1045				1050						1055		
TCC	CCT	TTG	TCT	CAT	GCT	CAA	TTA	ATG	TTC	CCA	GCA	CCA	TCA	GCC	CCT	3216
Ser	Pro	Leu	Ser	His	Ala	Gln	Leu	Met	Phe	Pro	Ala	Pro	Ser	Ala	Pro	
			1060					1065					1070			
TGT	TCC	TCT	GCC	CCG	TCT	GTC	CCA	GAT	ATT	TCT	AAG	CAC	AGA	CCC	CAG	3264
Cys	Ser	Ser	Ala	Pro	Ser	Val	Pro	Asp	Ile	Ser	Lys	His	Arg	Pro	Gln	
		1075					1080					1085				
GCA	TTT	GTT	CCC	TGC	AAA	ATA	CCT	TCC	GCA	TCT	CCT	CAG	ACA	CAG	CGC	3312
Ala	Phe	Val	Pro	Cys	Lys	Ile	Pro	Ser	Ala	Ser	Pro	Gln	Thr	Gln	Arg	
	1090						1095				1100					
AAG	TTC	TCT	CTA	CAA	TTC	CAG	AGG	AAC	TGC	TCT	GAA	CAC	CGA	GAC	TCA	3360
Lys	Phe	Ser	Leu	Gln	Phe	Gln	Arg	Asn	Cys	Ser	Glu	His	Arg	Asp	Ser	
	1105					1110				1115					1120	
GAC	CAG	CTC	TCC	CCA	GTC	TTC	ACT	CAG	TCA	AGA	CCC	CCA	CCC	TCC	AGT	3408
Asp	Gln	Leu	Ser	Pro	Val	Phe	Thr	Gln	Ser	Arg	Pro	Pro	Pro	Ser	Ser	
				1125					1130					1135		

000090-06280960

Lys His Pro Val Phe Arg Thr Thr Trp
1585 1590

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 466..2325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGGCGGCC	GCTCTAGAAC	TAGTGGATCC	CCCGGGCTGC	AGGAATTCGG	CACGAGGGAC		60
GATCCAGCGG	CAGAGTCGCC	GCTTCCGCTT	CGCTGCTTCT	CCGGTCGGCG	ACGCGGGCCC		120
GGGGCTTCCT	TTTCATCGGC	CCAGCTTATT	CCGCGGGCCC	CGGGGCTGCA	GCTACCCAGA		180
AGCGGCGAAG	AGGCCCTGGG	CTGCGCGCCC	GCTGTCCCAT	GTGAAGCAGG	TTGGGCCTGG		240
TCCCCGGCCC	GTGCCC GGTT	GTCTGCGGCC	CTTCAGGCCT	CAGGGACCCC	CGCGAGGCGC		300
TGCTCCTGGG	GGGCGCGGTG	ACAGGCCGTG	CGGGGGCGGA	GGGGCCAGCT	CGGTGGCCTC		360
CTCTCGGCCC	TCGCGTCCGC	GATCCCGCCC	AGCGGCCGGG	CAATAAAGAA	TGTTGATGGG		420
AGAACCATTT	TCCTAATTTT	CAAATTATTG	AGCTGGTCGC	GCATA ATG GAT GAT			474
				Met Asp Asp			
				1			
CAG CAA GCT TTG AAT TCA ATC ATG CAA GAT TTG	GCT GTC CTT CAT AAG						522
Gln Gln Ala Leu Asn Ser Ile Met Gln Asp Leu	Ala Val Leu His Lys						
5	10	15					
CCA GTC GGC CAG CAT TAT CTT TAC AAG AAA CCA GGA AAG CAA AAC CTT							570
Pro Val Gly Gln His Tyr Leu Tyr Lys Lys Pro Gly Lys Gln Asn Leu							
20	25	30	35				

Glu Leu Leu Arg His Met Phe Val His Tyr His
610 615

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 466..2325
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTGGCGGCC	GCTCTAGAAC	TAGTGGATCC	CCCGGGCTGC	AGGAATTCGG	CACGAGGGAC		60
GATCCAGCGG	CAGAGTCGCC	GCTTCCGCTT	CGCTGCTTCT	CCGGTCGGCG	ACGCGGGCCC		120
GGGGCTTCCT	TTTCATCGGC	CCAGCTTATT	CCGCGGGCCC	CGGGGCTGCA	GCTACCCAGA		180
AGCGGCGAAG	AGGCCCTGGG	CTGCGCGCCC	GCTGTCCCAT	GTGAAGCAGG	TTGGGCCTGG		240
TCCCCGGCCC	GTGCCC GGTT	GTCTGCGGCC	CTTCAGGCCT	CAGGGACCCC	CGCGAGGCGC		300
TGCTCCTGGG	GGGCGCGGTG	ACAGGCCGTG	CGGGGGCGGA	GGGGCCAGCT	CGGTGGCCTC		360
CTCTCGGCCC	TCGCGTCCGC	GATCCCGCCC	AGCGGCCGGG	CAATAAAGAA	TGTTGATGGG		420
AGAACCATTT	TCCTAATTTT	CAAATTATTG	AGCTGGTCGC	GCATA ATG GAT GAT			474
				Met Asp Asp			
				1			
CAG CAA GCT TTG AAT TCA ATC ATG CAA GAT TTG GCT GTC CTT CAT AAG							522
Gln Gln Ala Leu Asn Ser Ile Met Gln Asp Leu Ala Val Leu His Lys							
5			10			15	
GCC AGT CGG CCA GCA TTA TCT TTA CAA GAA ACC AGG AAA GCA AAA CCT							570
Ala Ser Arg Pro Ala Leu Ser Leu Gln Glu Thr Arg Lys Ala Lys Pro							
20			25			30	35
TCA TCA CCA AAA AAA CAG AAT GAT GTT CGA GTC AAA TTT GAA CAT AGA							618
Ser Ser Pro Lys Lys Gln Asn Asp Val Arg Val Lys Phe Glu His Arg							
			40			45	50

Leu	His	Lys	Ala	Ser	Arg	Pro	Ala	Leu	Ser	Leu	Gln	Glu	Thr	Arg	Lys	
			20					25					30			
Ala	Lys	Pro	Ser	Ser	Pro	Lys	Lys	Gln	Asn	Asp	Val	Arg	Val	Lys	Phe	
			35					40					45			
Glu	His	Arg	Gly	Glu	Lys	Arg	Ile	Leu	Gln	Val	Thr	Arg	Pro	Val	Lys	
			50					55					60			
Leu	Glu	Asp	Leu	Arg	Ser	Lys	Ser	Lys	Ile	Ala	Phe	Gly	Gln	Ser	Met	
			65					70					75		80	
Asp	Leu	His	Tyr	Thr	Asn	Asn	Glu	Leu	Val	Ile	Pro	Leu	Thr	Thr	Gln	
			85					90					95			
Asp	Asp	Leu	Asp	Lys	Ala	Val	Glu	Leu	Leu	Asp	Arg	Ser	Ile	His	Met	
			100					105					110			
Lys	Ser	Leu	Lys	Ile	Leu	Leu	Val	Val	Asn	Gly	Ser	Thr	Gln	Ala	Thr	
			115					120					125			
Asn	Leu	Glu	Pro	Ser	Pro	Ser	Pro	Glu	Asp	Leu	Asn	Asn	Thr	Pro	Leu	
			130					135					140			
Gly	Ala	Glu	Arg	Lys	Lys	Arg	Leu	Ser	Val	Val	Gly	Pro	Pro	Asn	Arg	
			145					150					155		160	
Asp	Arg	Ser	Ser	Pro	Pro	Pro	Gly	Tyr	Ile	Pro	Asp	Ile	Leu	His	Gln	
			165					170					175			
Ile	Ala	Arg	Asn	Gly	Ser	Phe	Thr	Ser	Ile	Asn	Ser	Glu	Gly	Glu	Phe	
			180					185					190			
Ile	Pro	Glu	Ser	Met	Asp	Gln	Met	Leu	Asp	Pro	Leu	Ser	Leu	Ser	Ser	
			195					200					205			
Pro	Glu	Asn	Ser	Gly	Ser	Gly	Ser	Cys	Pro	Ser	Leu	Asp	Ser	Pro	Leu	
			210					215					220			
Asp	Gly	Glu	Ser	Tyr	Pro	Lys	Ser	Arg	Met	Pro	Arg	Ala	Gln	Ser	Tyr	
			225					230					235		240	
Pro	Asp	Asn	His	Gln	Glu	Phe	Thr	Asp	Tyr	Asp	Asn	Pro	Ile	Phe	Glu	
			245					250					255			
Lys	Phe	Gly	Lys	Gly	Gly	Thr	Tyr	Pro	Arg	Arg	Tyr	His	Val	Ser	Tyr	
			260					265					270			
His	His	Gln	Glu	Tyr	Asn	Asp	Gly	Arg	Lys	Thr	Phe	Pro	Arg	Ala	Arg	
			275					280					285			
Arg	Thr	Gln	Gly	Thr	Ser	Phe	Arg	Ser	Pro	Val	Ser	Phe	Ser	Pro	Thr	
			290					295					300			

Glu Leu Leu Arg His Met Phe Val His Tyr His
610 615

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3089 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 400..2280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGGGAACAAA	AGCTGGAGCT	CCACCGCGGT	GGCGGCCGCT	CTAGAACTAG	TGGATCCCCC		60										
GGGCTGCAGG	AATTCGGCAC	GAGGAACAGT	GGCCGGTCGG	AGCGTCTTCT	GGACTTCAGG		120										
ACTCGCAGGC	GGCCCGGTCG	AGTGGCGCCG	CCGAGGCCGG	GTTGGGCCGA	GCCTGGGAGC		180										
GCCGGGGATG	TAGCGGGCCA	ACCTGCTCAT	GCCACAGCGC	CCGGCCGCGG	CCGAGCCGGA		240										
GCCTGGGGAG	GCGGCGGGGG	CCCCGAGCGC	AGCCACGGC	CCCCGCGCGG	AGCCAGGCCC		300										
GCTGCCGTCC	CCGCCGCCCG	CTCCCCCGGC	ATGCAGCCCC	GGCTGCGGAG	GTGACACTTC		360										
TGGGCTGTAG	TCGCCACCGC	CGCCTCCGCC	ATCGCCACC	ATG	GAT	GAA	CAA	GAG		414							
				Met	Asp	Glu	Gln	Glu									
				1				5									
GCA	TTA	GAC	TCG	ATC	ATG	AAG	GAC	CTG	GTG	GCC	CTC	CAG	ATG	AGC	CGA		462
Ala	Leu	Asp	Ser	Ile	Met	Lys	Asp	Leu	Val	Ala	Leu	Gln	Met	Ser	Arg		
				10					15					20			
CGA	ACC	CGG	TTG	TCT	GGA	TAT	GAG	ACC	ATG	AAG	AAT	AAG	GAC	ACA	GGT		510
Arg	Thr	Arg	Leu	Ser	Gly	Tyr	Glu	Thr	Met	Lys	Asn	Lys	Asp	Thr	Gly		
			25					30					35				
CAC	CCA	AAC	AGG	CAG	AGT	GAC	GTC	AGA	ATC	AAG	TTT	GAA	CAC	AAT	GGG		558
His	Pro	Asn	Arg	Gln	Ser	Asp	Val	Arg	Ile	Lys	Phe	Glu	His	Asn	Gly		
			40					45				50					
GAG	AGA	CGA	ATT	ATA	GCA	TTC	AGC	CGG	CCT	GTG	AGA	TAC	GAA	GAT	GTG		606
Glu	Arg	Arg	Ile	Ile	Ala	Phe	Ser	Arg	Pro	Val	Arg	Tyr	Glu	Asp	Val		
			55				60				65						

ACA	TTT	CCC	CGA	ATA	CGA	CGG	CAT	CAA	GGC	AAC	CTA	TTC	ACT	CTG	GTG	1326
Thr	Phe	Pro	Arg	Ile	Arg	Arg	His	Gln	Gly	Asn	Leu	Phe	Thr	Leu	Val	
	295					300					305					
CCC	TCA	AGT	CGC	TCC	TTG	AGC	ACA	AAT	GGC	GAG	AAC	ATG	GGT	GTA	GCT	1374
Pro	Ser	Ser	Arg	Ser	Leu	Ser	Thr	Asn	Gly	Glu	Asn	Met	Gly	Val	Ala	
310					315					320					325	
GTG	CAA	TAC	CTG	GAC	CCC	CGT	GGG	CGC	CTA	CGG	AGT	GCA	GAC	AGT	GAG	1422
Val	Gln	Tyr	Leu	Asp	Pro	Arg	Gly	Arg	Leu	Arg	Ser	Ala	Asp	Ser	Glu	
				330					335					340		
AAT	GCC	CTC	ACT	GTG	CAG	GAA	AGG	AAT	GTG	CCA	ACC	AAA	TCT	CCT	AGT	1470
Asn	Ala	Leu	Thr	Val	Gln	Glu	Arg	Asn	Val	Pro	Thr	Lys	Ser	Pro	Ser	
			345					350					355			
GCT	CCC	ATC	AAT	TGG	CGT	CGG	GGG	AAG	CTC	CTG	GGT	CAA	GGT	GCC	TTC	1518
Ala	Pro	Ile	Asn	Trp	Arg	Arg	Gly	Lys	Leu	Leu	Gly	Gln	Gly	Ala	Phe	
		360					365					370				
GGC	AGG	GTC	TAC	TTG	TGC	TAT	GAT	GTG	GAC	ACA	GGA	CGT	GAA	CTT	GCT	1566
Gly	Arg	Val	Tyr	Leu	Cys	Tyr	Asp	Val	Asp	Thr	Gly	Arg	Glu	Leu	Ala	
	375					380					385					
TCT	AAG	CAG	GTC	CAG	TTT	GAC	CCA	GAT	AGT	CCT	GAG	ACA	AGC	AAG	GAG	1614
Ser	Lys	Gln	Val	Gln	Phe	Asp	Pro	Asp	Ser	Pro	Glu	Thr	Ser	Lys	Glu	
390					395					400					405	
GTG	AGT	GCT	CTG	GAG	TGT	GAG	ATC	CAG	TTG	CTG	AAG	AAC	CTG	CAG	CAT	1662
Val	Ser	Ala	Leu	Glu	Cys	Glu	Ile	Gln	Leu	Leu	Lys	Asn	Leu	Gln	His	
				410					415					420		
GAG	CGC	ATT	GTG	CAG	TAC	TAC	GGC	TGC	CTG	CGG	GAC	CGT	GCT	GAG	AAG	1710
Glu	Arg	Ile	Val	Gln	Tyr	Tyr	Gly	Cys	Leu	Arg	Asp	Arg	Ala	Glu	Lys	
			425				430						435			
ATC	CTC	ACC	ATC	TTT	ATG	GAG	TAT	ATG	CCA	GGG	GGC	TCT	GTA	AAA	GAC	1758
Ile	Leu	Thr	Ile	Phe	Met	Glu	Tyr	Met	Pro	Gly	Gly	Ser	Val	Lys	Asp	
		440					445					450				
CAG	TTG	AAG	GCC	TAC	GGA	GCT	CTG	ACA	GAG	AGT	GTG	ACC	CGC	AAG	TAC	1806
Gln	Leu	Lys	Ala	Tyr	Gly	Ala	Leu	Thr	Glu	Ser	Val	Thr	Arg	Lys	Tyr	
	455					460					465					
ACC	CGG	CAG	ATT	CTG	GAG	GGC	ATG	TCA	TAC	CTG	CAC	AGC	AAC	ATG	ATT	1854
Thr	Arg	Gln	Ile	Leu	Glu	Gly	Met	Ser	Tyr	Leu	His	Ser	Asn	Met	Ile	
470					475					480					485	
GTG	CAT	CGG	GAC	ATC	AAG	GGA	GCC	AAT	ATC	CTC	CGA	GAC	TCA	GCT	GGG	1902
Val	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu	Arg	Asp	Ser	Ala	Gly	
				490					495					500		

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met 1	Asp	Glu	Gln	Glu	Ala	Leu	Asp	Ser	Ile	Met	Lys	Asp	Leu	Val	Ala	
				5					10					15		
Leu	Gln	Met	Ser	Arg	Arg	Thr	Arg	Leu	Ser	Gly	Tyr	Glu	Thr	Met	Lys	
				20				25					30			
Asn	Lys	Asp	Thr	Gly	His	Pro	Asn	Arg	Gln	Ser	Asp	Val	Arg	Ile	Lys	
				35			40					45				
Phe	Glu	His	Asn	Gly	Glu	Arg	Arg	Ile	Ile	Ala	Phe	Ser	Arg	Pro	Val	
				50		55					60					
Arg	Tyr	Glu	Asp	Val	Glu	His	Lys	Val	Thr	Thr	Val	Phe	Gly	Gln	Pro	
65					70				75					80		
Leu	Asp	Leu	His	Tyr	Met	Asn	Asn	Glu	Leu	Ser	Ile	Leu	Leu	Lys	Asn	
				85				90					95			
Gln	Asp	Asp	Leu	Asp	Lys	Ala	Ile	Asp	Ile	Leu	Asp	Arg	Ser	Ser	Ser	
				100				105					110			
Met	Lys	Ser	Leu	Arg	Ile	Leu	Leu	Leu	Ser	Gln	Asp	Arg	Asn	His	Thr	
				115			120					125				
Ser	Ser	Ser	Pro	His	Ser	Gly	Val	Ser	Arg	Gln	Val	Arg	Ile	Lys	Pro	
				130		135					140					
Ser	Gln	Ser	Ala	Gly	Asp	Ile	Asn	Thr	Ile	Tyr	Gln	Ala	Pro	Glu	Pro	
145					150				155					160		
Arg	Ser	Arg	His	Leu	Ser	Val	Ser	Ser	Gln	Asn	Pro	Gly	Arg	Ser	Ser	
				165				170					175			
Pro	Pro	Pro	Gly	Tyr	Val	Pro	Glu	Arg	Gln	Gln	His	Ile	Ala	Arg	Gln	
				180				185					190			
Gly	Ser	Tyr	Thr	Ser	Ile	Asn	Ser	Glu	Gly	Glu	Phe	Ile	Pro	Glu	Thr	
				195			200					205				
Ser	Glu	Gln	Cys	Met	Leu	Asp	Pro	Leu	Ser	Ser	Ala	Glu	Asn	Ser	Leu	
				210		215					220					
Ser	Gly	Ser	Cys	Gln	Ser	Leu	Asp	Arg	Ser	Ala	Asp	Ser	Pro	Ser	Phe	
225					230				235					240		

TGTAGCGCTG	TGTCCTGGGA	AGAACTGAGA	GCCATGGACC	TGCCTTCCTT	TGAGCCCCGC	600
TTCCTGGTGC	TCTGTGGGT	CCTGCTGAAC	GTGATCCACG	AGTGCCTGAA	GCTGCGGCTG	660
GAACAGAGGC	TGCCGGGGAG	CCTTCCCTCT	TGAGTATCAA	ACAGCTAGTG	CGAGAGTGTA	720
AAGAGGTCCT	AAAGGGCGGG	CTCCTG	ATG AAG CAG TAT TAC CAG TTC ATG CTG			773
			Met Lys Gln Tyr Tyr Gln Phe Met Leu			
		1		5		
CAG GAG GTC CTG GGC GGA CTG GAG AAG ACC GAC TGC AAC ATG GAT GCC						821
Gln Glu Val Leu Gly Gly Leu Glu Lys Thr Asp Cys Asn Met Asp Ala						
10		15		20	25	
TTT GAG GAG GAC CTG CAG AAG ATG CTG ATG GTG TAT TTT GAT TAC ATG						869
Phe Glu Glu Asp Leu Gln Lys Met Leu Met Val Tyr Phe Asp Tyr Met						
	30		35		40	
AGA AGC TGG ATC CAA ATG CTA CAG CAG TTA CCT CAG GCT TCC CAT AGC						917
Arg Ser Trp Ile Gln Met Leu Gln Gln Leu Pro Gln Ala Ser His Ser						
	45		50		55	
TTA AAA AAC CTG CTA GAA GAG GAA TGG AAT TTC ACC AAA GAA ATA ACC						965
Leu Lys Asn Leu Leu Glu Glu Glu Trp Asn Phe Thr Lys Glu Ile Thr						
	60		65		70	
CAT TAT ATC CGT GGC GGA GAA GCG CAG GCT GGA AAG CTT TTC TGT GAC						1013
His Tyr Ile Arg Gly Gly Glu Ala Gln Ala Gly Lys Leu Phe Cys Asp						
	75		80		85	
ATC GCA GGG ATG CTG CTG AAA TCC ACA GGG AGC TTT CTG GAA TCC GGC						1061
Ile Ala Gly Met Leu Leu Lys Ser Thr Gly Ser Phe Leu Glu Ser Gly						
90		95		100	105	
CTG CAG GAG AGC TGT GCT GAG CTG TGG ACC AGN GCC GAC GAC AAC GGT						1109
Leu Gln Glu Ser Cys Ala Glu Leu Trp Thr XAA Ala Asp Asp Asn Gly						
	110		115		120	
GCT GCC GAC GAG CTA AGG AGA TCT GTC ATC GAG ATC AGC CGA GCA CTC						1157
Ala Ala Asp Glu Leu Arg Arg Ser Val Ile Glu Ile Ser Arg Ala Leu						
	125		130		135	
AAG GAG CTC TTC CAC GAA GCC AGG GAA AGA GCC TCC AAG GCC CTG GGC						1205
Lys Glu Leu Phe His Glu Ala Arg Glu Arg Ala Ser Lys Ala Leu Gly						
	140		145		150	
TTT GCT AAA ATG CTG AGG AAG GAC CTA GAA ATA GCA GCA GAG TTC GTG						1253
Phe Ala Lys Met Leu Arg Lys Asp Leu Glu Ile Ala Ala Glu Phe Val						
	155		160		165	
CTA TCT GCA TCA GCC CGA GAG CTC CTG GAC GCT CTG AAA GCA AAG CAG						1301
Leu Ser Ala Ser Ala Arg Glu Leu Leu Asp Ala Leu Lys Ala Lys Gln						
170		175		180	185	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 127..4917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGGCTCCTG CGGCGGGCTA GAGGCGGAGG CGGAGTCGAG TCACTCCCTC ACCCGCGGC	60
TCCTGGTCTT CCCGCACCAG GCTGCAGCTG ACGACCCGCC GCGGTCATGC GAAGCTTGAT	120
GCACGG ATG AGA GAC GCC ATC GCC GAG CCG GTG CCC CCT CCT GCC CTC	168
Met Arg Asp Ala Ile Ala Glu Pro Val Pro Pro Pro Ala Leu	
1 5 10	
GCC GAC ACC CCT GCA GCC GCC ATG GAG GAG CTG CGG CCA GCA CCG CCG	216
Ala Asp Thr Pro Ala Ala Ala Met Glu Glu Leu Arg Pro Ala Pro Pro	
15 20 25 30	
CCA CAG CCC GAG CCG GAT CCG GAG TGC TGC CCA GCG GCG AGG CAG GAG	264
Pro Gln Pro Glu Pro Asp Pro Glu Cys Cys Pro Ala Ala Arg Gln Glu	
35 40 45	
TGC ATG TTG GGA GAG TCG GCT CGC AAA AGT ATG GAA TCC GAT CCA GAG	312
Cys Met Leu Gly Glu Ser Ala Arg Lys Ser Met Glu Ser Asp Pro Glu	
50 55 60	
GAC TTT TCT GAT GAA ACA AAT ACA GAG ACT CTC TAC GGC ACC TCA CCC	360
Asp Phe Ser Asp Glu Thr Asn Thr Glu Thr Leu Tyr Gly Thr Ser Pro	
65 70 75	
CCA AGC ACA CCT CGA CAG ATG AAA CGC CTG TCA GCC AAG CAC CAG AGG	408
Pro Ser Thr Pro Arg Gln Met Lys Arg Leu Ser Ala Lys His Gln Arg	
80 85 90	
AAC AGC GCA GGG AGG CCG GCC AGC CGA TCG AAC TTG AAA GAA AAA ATG	456
Asn Ser Ala Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu Lys Met	
95 100 105 110	
AAC ACA CCG AGT CAG TCT CCA CAT AAA GAT TTG GGG AAG GGA GTG GAG	504
Asn Thr Pro Ser Gln Ser Pro His Lys Asp Leu Gly Lys Gly Val Glu	
115 120 125	
ACC GTG GAA GAA TAC AGC TAC AAG CAG GAG AAG AAG ATT CGA GCA ACT	552
Thr Val Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg Ala Thr	
130 135 140	
CTG AGA ACA ACG GAG CGA GAC CAT AAG AAA AAT GCA CAG TGC TCA TTC	600
Leu Arg Thr Thr Glu Arg Asp His Lys Lys Asn Ala Gln Cys Ser Phe	
145 150 155	

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ATG	TTG	GAC	TCG	GTG	GCT	GGG	TCT	TTG	CCA	AAA	AAA	TCG	ATT	CCA	GAT	648
Met	Leu	Asp	Ser	Val	Ala	Gly	Ser	Leu	Pro	Lys	Lys	Ser	Ile	Pro	Asp	
	160					165					170					
GTG	GAT	CTC	AAT	AAG	CCT	TAC	CTC	AGT	CTC	GGC	TGT	AGC	AAT	GCC	AAG	696
Val	Asp	Leu	Asn	Lys	Pro	Tyr	Leu	Ser	Leu	Gly	Cys	Ser	Asn	Ala	Lys	
175					180					185					190	
CTG	CCC	GTC	TCG	ATG	CCC	ATG	CCG	ATA	GCC	AGA	ACT	GCA	CGG	CAG	ACT	744
Leu	Pro	Val	Ser	Met	Pro	Met	Pro	Ile	Ala	Arg	Thr	Ala	Arg	Gln	Thr	
				195					200					205		
TCC	CGG	ACT	GAC	TGC	CCC	GCA	GAT	CGC	TTA	AAG	TTC	TTT	GAA	ACA	CTG	792
Ser	Arg	Thr	Asp	Cys	Pro	Ala	Asp	Arg	Leu	Lys	Phe	Phe	Glu	Thr	Leu	
			210					215					220			
CGC	CTT	TTG	CTA	AAG	CTT	ACC	TCA	GTC	TCG	AAG	AAG	AAG	GAC	AGG	GAG	840
Arg	Leu	Leu	Leu	Lys	Leu	Thr	Ser	Val	Ser	Lys	Lys	Lys	Asp	Arg	Glu	
	225						230					235				
CAG	AGG	GGA	CAA	GAA	AAC	ACG	GCT	GCT	TTC	TGG	TTC	AAC	CGA	TCG	AAC	888
Gln	Arg	Gly	Gln	Glu	Asn	Thr	Ala	Ala	Phe	Trp	Phe	Asn	Arg	Ser	Asn	
	240					245					250					
GAA	CTG	ATC	TGG	TTA	GAA	CTG	CAG	GCC	TGG	CAC	GCG	GGC	CGC	ACC	ATC	936
Glu	Leu	Ile	Trp	Leu	Glu	Leu	Gln	Ala	Trp	His	Ala	Gly	Arg	Thr	Ile	
255					260				265						270	
AAT	GAC	CAG	GAC	CTC	TTT	CTC	TAC	ACA	GCC	CGC	CAG	GCC	ATC	CCA	GAC	984
Asn	Asp	Gln	Asp	Leu	Phe	Leu	Tyr	Thr	Ala	Arg	Gln	Ala	Ile	Pro	Asp	
				275					280					285		
ATC	ATC	AAT	GAG	ATC	CTC	ACC	TTC	AAA	GTT	AAC	TAC	GGG	AGC	ATT	GCC	1032
Ile	Ile	Asn	Glu	Ile	Leu	Thr	Phe	Lys	Val	Asn	Tyr	Gly	Ser	Ile	Ala	
			290					295					300			
TTC	TCC	AGC	AAT	GGA	GCC	GGT	TTC	AAC	GGG	CCC	TTG	GTA	GAA	GGC	CAG	1080
Phe	Ser	Ser	Asn	Gly	Ala	Gly	Phe	Asn	Gly	Pro	Leu	Val	Glu	Gly	Gln	
		305					310					315				
TGC	AGA	ACC	CCT	CAG	GAG	ACA	AAC	CGT	GTG	GGC	TGC	TCA	TCG	TAC	CAC	1128
Cys	Arg	Thr	Pro	Gln	Glu	Thr	Asn	Arg	Val	Gly	Cys	Ser	Ser	Tyr	His	
	320					325					330					
GAG	CAC	CTC	CAG	CGC	CAG	AGG	GTC	TCG	TTT	GAG	CAG	GTG	AAG	CGG	ATA	1176
Glu	His	Leu	Gln	Arg	Gln	Arg	Val	Ser	Phe	Glu	Gln	Val	Lys	Arg	Ile	
335					340					345					350	
ATG	GAG	CTG	CTG	GAG	TAC	ATG	GAG	GCA	CTT	TAC	CCA	TCC	TTG	CAG	GCT	1224
Met	Glu	Leu	Leu	Glu	Tyr	Met	Glu	Ala	Leu	Tyr	Pro	Ser	Leu	Gln	Ala	
				355					360					365		
CT																

TTC	CTG	GTG	CTC	TGT	CGG	GTC	CTG	CTG	AAC	GTG	ATC	CAC	GAG	TGC	CTG	1992
Phe	Leu	Val	Leu	Cys	Arg	Val	Leu	Leu	Asn	Val	Ile	His	Glu	Cys	Leu	
		610						615					620			
AAG	CTG	CGG	CTG	GAA	CAG	AGG	CCT	GCC	GGG	GAG	CCT	TCC	CTC	TTG	AGT	2040
Lys	Leu	Arg	Leu	Glu	Gln	Arg	Pro	Ala	Gly	Glu	Pro	Ser	Leu	Leu	Ser	
		625					630					635				
ATC	AAA	CAG	CTA	GTG	CGA	GAG	TGT	AAA	GAG	GTC	CTA	AAG	GGC	GGG	CTC	2088
Ile	Lys	Gln	Leu	Val	Arg	Glu	Cys	Lys	Glu	Val	Leu	Lys	Gly	Gly	Leu	
	640					645					650					
CTG	ATG	AAG	CAG	TAT	TAC	CAG	TTC	ATG	CTG	CAG	GAG	GTC	CTG	GGC	GGA	2136
Leu	Met	Lys	Gln	Tyr	Tyr	Gln	Phe	Met	Leu	Gln	Glu	Val	Leu	Gly	Gly	
655					660					665					670	
CTG	GAG	AAG	ACC	GAC	TGC	AAC	ATG	GAT	GCC	TTT	GAG	GAG	GAC	CTG	CAG	2184
Leu	Glu	Lys	Thr	Asp	Cys	Asn	Met	Asp	Ala	Phe	Glu	Glu	Asp	Leu	Gln	
			675						680					685		
AAG	ATG	CTG	ATG	GTG	TAT	TTT	GAT	TAC	ATG	AGA	AGC	TGG	ATC	CAA	ATG	2232
Lys	Met	Leu	Met	Val	Tyr	Phe	Asp	Tyr	Met	Arg	Ser	Trp	Ile	Gln	Met	
		690						695					700			
CTA	CAG	CAG	TTA	CCT	CAG	GCT	TCC	CAT	AGC	TTA	AAA	AAC	CTG	CTA	GAA	2280
Leu	Gln	Gln	Leu	Pro	Gln	Ala	Ser	His	Ser	Leu	Lys	Asn	Leu	Leu	Glu	
		705					710					715				
GAG	GAA	TGG	AAT	TTC	ACC	AAA	GAA	ATA	ACC	CAT	TAT	ATC	CGT	GGC	GGA	2328
Glu	Glu	Trp	Asn	Phe	Thr	Lys	Glu	Ile	Thr	His	Tyr	Ile	Arg	Gly	Gly	
	720					725					730					
GAA	GCG	CAG	GCT	GGA	AAG	CTT	TTC	TGT	GAC	ATC	GCA	GGG	ATG	CTG	CTG	2376
Glu	Ala	Gln	Ala	Gly	Lys	Leu	Phe	Cys	Asp	Ile	Ala	Gly	Met	Leu	Leu	
735				740						745					750	
AAA	TCC	ACA	GGG	AGC	TTT	CTG	GAA	TCC	GGC	CTG	CAG	GAG	AGC	TGT	GCT	2424
Lys	Ser	Thr	Gly	Ser	Phe	Leu	Glu	Ser	Gly	Leu	Gln	Glu	Ser	Cys	Ala	
			755						760					765		
GAG	CTG	TGG	ACC	AGC	GCC	GAC	GAC	AAC	GGT	GCT	GCC	GAC	GAG	CTA	AGG	2472
Glu	Leu	Trp	Thr	Ser	Ala	Asp	Asp	Asn	Gly	Ala	Ala	Asp	Glu	Leu	Arg	
			770					775					780			
AGA	TCT	GTC	ATC	GAG	ATC	AGC	CGA	GCA	CTC	AAG	GAG	CTC	TTC	CAC	GAA	2520
Arg	Ser	Val	Ile	Glu	Ile	Ser	Arg	Ala	Leu	Lys	Glu	Leu	Phe	His	Glu	
		785					790					795				
GCC	AGG	GAA	AGA	GCC	TCC	AAG	GCC	CTG	GGC	TTT	GCT	AAA	ATG	CTG	AGG	2568
Ala	Arg	Glu	Arg	Ala	Ser	Lys	Ala	Leu	Gly	Phe	Ala	Lys	Met	Leu	Arg	

Thr	Pro	Ala	Ala	Ala	Met	Glu	Glu	Leu	Arg	Pro	Ala	Pro	Pro	Pro	Gln	
			20				25						30			
Pro	Glu	Pro	Asp	Pro	Glu	Cys	Cys	Pro	Ala	Ala	Arg	Gln	Glu	Cys	Met	
			35				40						45			
Leu	Gly	Glu	Ser	Ala	Arg	Lys	Ser	Met	Glu	Ser	Asp	Pro	Glu	Asp	Phe	
			50				55						60			
Ser	Asp	Glu	Thr	Asn	Thr	Glu	Thr	Leu	Tyr	Gly	Thr	Ser	Pro	Pro	Ser	
			65				70						80			
Thr	Pro	Arg	Gln	Met	Lys	Arg	Leu	Ser	Ala	Lys	His	Gln	Arg	Asn	Ser	
			85						90						95	
Ala	Gly	Arg	Pro	Ala	Ser	Arg	Ser	Asn	Leu	Lys	Glu	Lys	Met	Asn	Thr	
			100						105						110	
Pro	Ser	Gln	Ser	Pro	His	Lys	Asp	Leu	Gly	Lys	Gly	Val	Glu	Thr	Val	
			115						120						125	
Glu	Glu	Tyr	Ser	Tyr	Lys	Gln	Glu	Lys	Lys	Ile	Arg	Ala	Thr	Leu	Arg	
			130						135						140	
Thr	Thr	Glu	Arg	Asp	His	Lys	Lys	Asn	Ala	Gln	Cys	Ser	Phe	Met	Leu	
			145						150						155	
Asp	Ser	Val	Ala	Gly	Ser	Leu	Pro	Lys	Lys	Ser	Ile	Pro	Asp	Val	Asp	
			165						170						175	
Leu	Asn	Lys	Pro	Tyr	Leu	Ser	Leu	Gly	Cys	Ser	Asn	Ala	Lys	Leu	Pro	
			180						185						190	
Val	Ser	Met	Pro	Met	Pro	Ile	Ala	Arg	Thr	Ala	Arg	Gln	Thr	Ser	Arg	
			195						200						205	
Thr	Asp	Cys	Pro	Ala	Asp	Arg	Leu	Lys	Phe	Phe	Glu	Thr	Leu	Arg	Leu	
			210						215						220	
Leu	Leu	Lys	Leu	Thr	Ser	Val	Ser	Lys	Lys	Lys	Asp	Arg	Glu	Gln	Arg	
			225						230						235	
Gly	Gln	Glu	Asn	Thr	Ala	Ala	Phe	Trp	Phe	Asn	Arg	Ser	Asn	Glu	Leu	
			245						250						255	
Ile	Trp	Leu	Glu	Leu	Gln	Ala	Trp	His	Ala	Gly	Arg	Thr	Ile	Asn	Asp	
			260						265						270	
Gln	Asp	Leu	Phe	Leu	Tyr	Thr	Ala	Arg	Gln	Ala	Ile	Pro	Asp	Ile	Ile	
			275						280						285	
Asn	Glu	Ile	Leu	Thr	Phe	Lys	Val	Asn	Tyr	Gly	Ser	Ile	Ala	Phe	Ser	
			290						295						300	

